Proteomics-2013
OMICS Group Conferences
Accelerating Scientific Discovery
3rd International Conference on
Proteomics & Bioinformatics
July 15-17, 2013 Courtyard by Marriott Philadelphia Downtown, USA

A comprehensive proteomic and epigenomic analysis of FFPE patient melanoma

Alan Tackett
University of Arkansas for Medical Sciences, USA

Abstract

Molecular pathways regulating melanoma initiation and progression are potential targets of therapeutic development for this aggressive cancer. We present the most comprehensive analysis of formalin-fixed paraffin-embedded human melanoma tissues using quantitative proteomics. From 61 patient samples, we identified 171 proteins varying in abundance among benign nevi, primary melanoma, and metastatic melanoma. Seventy-three percent of these proteins were validated by immunohistochemistry staining of malignant melanoma tissues from the Human Protein Atlas database. Our results reveal that molecular pathways involved with tumor cell proliferation, motility, and apoptosis are mis-regulated in melanoma. These data provide the most comprehensive proteome resource on patient melanoma and reveal insight into the molecular mechanisms driving melanoma progression. Furthermore, we have used this quantitative mass spectrometry approach to uncover a panel of histone post-translational modifications that are differentially regulated in metastatic melanoma. This has allowed us to explore epigenomic mechanisms that regulate melanoma progression.

Biography

Alan Tackett laboratory focuses on histone epigenetic mechanisms that regulate gene transcription and that are coupled to melanoma progression. We utilize a suite of techniques in our studies including proteomics of human biopsies, immunohistochemistry, cell culture, tumorigenicity assays, ChIPseq, biochemical and proteomic approaches for analyses of protein complexes, and cutting-edge mass spectrometry for the analysis of histone post-translational modifications. We have a unique environment that provides for discovery-based studies like proteomics as well as hypothesis-driven studies like those we perform in cell culture and with skin biopsies. In addition to our melanoma work, we develop new technologies for epigenetic studies such as tools for detection of in vivo protein interactions and quantitative assays for histone modifying proteins.